RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/587,956 _____
Source: _____ IF,WP _____
Date Processed by STIC: _____ 08/14/2006 _____

ENTERED

IFWP

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RAW SEQUENCE LISTING                          DATE: 08/14/2006
PATENT APPLICATION:  US/10/587,956           TIME: 13:18:35

Input Set : A:\Sequence Listing.TXT
Output Set: N:\CRF4\08142006\J587956.raw
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```
 1 <110> APPLICANT: Korea Research Institute of Bioscience and Biotechnology
 3 <120> TITLE OF INVENTION: A novel Hansenula polymorpha gene coding for alpha 1,6
 4        mannosyltransferase and process for the production of recombinant
 5        glycoproteins with Hansenula polymorpha mutant strain deficient
 6        in the same gene
C-->  8 <140> CURRENT APPLICATION NUMBER: US/10/587,956
C-->  8 <141> CURRENT FILING DATE: 2006-07-31
W-->  0 <130> FILE REFERENCE:
 8 <160> NUMBER OF SEQ ID NOS: 14
10 <170> SOFTWARE: KopatentIn 1.71
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 1351
14 <212> TYPE: DNA
15 <213> ORGANISM: Hansenula polymorpha
17 <220> FEATURE:
18 <221> NAME/KEY: CDS
19 <222> LOCATION: (10)..(1293)
21 <400> SEQUENCE: 1
22 cggtgaaga atg gtg tat ttt tta aat ttc atg tca ata acc aat gtc ccg      51
23           Met Val Tyr Phe Leu Asn Phe Met Ser Ile Thr Asn Val Pro
24             1               5                  10
26 gtg ctg aag cgc gcg cga ctc tac atg gcg acg aat cgc cgg ctg gtg      99
27 Val Leu Lys Arg Ala Arg Leu Tyr Met Ala Thr Asn Arg Arg Leu Val
28  15                  20                  25                  30
30 gtt gtt ctt gtg gtg ctg ctg tac tgg gtg gtc cag aac gtt tgg acg     147
31 Val Val Leu Val Val Leu Leu Tyr Trp Val Val Gln Asn Val Trp Thr
32                  35                  40                  45
34 tgg agc cct ggg acg cgc gat ttg gcc caa gtg gac gcg aag atc gag     195
35 Trp Ser Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu
36                  50                  55                  60
38 gcc gag cta aac tcg aat cta cat act ttt gga gcg cat ttg cgc cac     243
39 Ala Glu Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His
40              65                  70                  75
42 tta aac cgg ctt ccg gca gag tcg gcc acc ctg cgt gaa aaa ctc acc     291
43 Leu Asn Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr
44          80                  85                  90
46 ttc tat ttc cca tat tat cct gaa aag ccc gtg ccg aac cag atc tgg     339
47 Phe Tyr Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp
48  95                 100                 105                 110
50 cag aca tgg aag gtc gat ctc gaa gac gac aac ttc ccc aag cag tac     387
51 Gln Thr Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr
52                 115                 120                 125
54 aga cgg ttt cag aag acg tgg gtc gag aaa aat cca gac tac gtg tac     435
```

```
55 Arg Arg Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr
56             130                 135                 140
58 cac ctg att ccg gac tct gtg att gag gac ttt gtg gcg agt ttg tac       483
59 His Leu Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr
60             145                 150                 155
62 gcg aac gtg ccg gag gtg gtc aga gcg tac cag ctg ctt ccg aaa aat       531
63 Ala Asn Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn
64             160                 165                 170
66 atc atg aag gcg gat ttt ttc cgg tat ttg gtg atc tac gcg cgc gga       579
67 Ile Met Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly
68 175                 180                 185                 190
70 ggc acc tac tca gac atg gac acg gtg tgt tta aag ccg atc aag gac       627
71 Gly Thr Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp
72             195                 200                 205
74 tgg gcc acg ttt gat cgc gac ctg atc cac gct gcc gac aat aag gcc       675
75 Trp Ala Thr Phe Asp Arg Asp Leu Ile His Ala Ala Asp Asn Lys Ala
76             210                 215                 220
78 gat ctc tcc cag ata gat cca gaa gca aga acc acg cct gtg ggg ctg       723
79 Asp Leu Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu
80             225                 230                 235
82 gtg att ggc att gag gcc gac ccg gac agg ccc gac tgg cac gag tgg       771
83 Val Ile Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His Glu Trp
84             240                 245                 250
86 ttc tcg cgc aga ctg cag ttc tgc cag tgg acg atc cag gcg aag ccg       819
87 Phe Ser Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro
88 255                 260                 265                 270
90 gga cac ccg ctg ctg cgc gag ctg atc atc cgg atc gtg gag gag acg       867
91 Gly His Pro Leu Leu Arg Glu Leu Ile Ile Arg Ile Val Glu Glu Thr
92             275                 280                 285
94 ttc cgc aaa cag cac atg ggc gtt ttg aaa aga gtg gaa ggc aag gac       915
95 Phe Arg Lys Gln His Met Gly Val Leu Lys Arg Val Glu Gly Lys Asp
96             290                 295                 300
98 tcg ggc gca gat atc atg cag tgg aca gga ccg ggg ata ttt aca gac       963
99 Ser Gly Ala Asp Ile Met Gln Trp Thr Gly Pro Gly Ile Phe Thr Asp
100            305                 310                 315
102 act ctg ttt gat tat ctg aac aat gtg gcg agc gac ggc aag ttg ggc     1011
103 Thr Leu Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly
104            320                 325                 330
106 gac ggg tac ggc gtg ggg tcg ttg tat tgg cgc aag cac ggc aaa tat     1059
107 Asp Gly Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr
108 335                 340                 345                 350
110 aag ctg aaa aag aca gaa att aac aag aat aac gag cca ttg cat tct     1107
111 Lys Leu Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser
112            355                 360                 365
114 gag gac cag ctt atc aac tgg agg tcg ctg acc aac atg gac aag cca     1155
115 Glu Asp Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro
116            370                 375                 380
118 aag atc atg ggg gac gta atg gtg tta cca atc acg agc ttt agt ccg     1203
119 Lys Ile Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro
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```
120         385             390             395
122 aac gtg ggg cac atg ggc tca aag agc agc tca gat agg ctg gca ttt      1251
123 Asn Val Gly His Met Gly Ser Lys Ser Ser Ser Asp Arg Leu Ala Phe
124     400             405             410
126 gtg gag cat tta ttt tct ggc agc tgg aag cca aaa aac aaa   taggaaa    1300
127 Val Glu His Leu Phe Ser Gly Ser Trp Lys Pro Lys Asn Lys
128 415             420             425
130 aataaataat tagctgcatt ttagataatt ctcatgagca ggcacagaac g            1351
133 <210> SEQ ID NO: 2
134 <211> LENGTH: 428
135 <212> TYPE: PRT
136 <213> ORGANISM: Hansenula polymorpha
138 <400> SEQUENCE: 2
139 Met Val Tyr Phe Leu Asn Phe Met Ser Ile Thr Asn Val Pro Val Leu
140   1             5               10              15
142 Lys Arg Ala Arg Leu Tyr Met Ala Thr Asn Arg Arg Leu Val Val Val
143             20              25              30
145 Leu Val Val Leu Leu Tyr Trp Val Val Gln Asn Val Trp Thr Trp Ser
146         35              40              45
148 Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu Ala Glu
149     50              55              60
151 Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His Leu Asn
152 65              70              75              80
154 Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr Phe Tyr
155             85              90              95
157 Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp Gln Thr
158             100             105             110
160 Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr Arg Arg
161         115             120             125
163 Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr His Leu
164     130             135             140
166 Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr Ala Asn
167 145             150             155             160
169 Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn Ile Met
170             165             170             175
172 Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly Gly Thr
173             180             185             190
175 Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp Trp Ala
176     195             200             205
178 Thr Phe Asp Arg Asp Leu Ile His Ala Ala Asp Asn Lys Ala Asp Leu
179     210             215             220
181 Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu Val Ile
182 225             230             235             240
184 Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His Glu Trp Phe Ser
185             245             250             255
187 Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro Gly His
188             260             265             270
190 Pro Leu Leu Arg Glu Leu Ile Ile Arg Ile Val Glu Glu Thr Phe Arg
191         275             280             285
```

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Input Set : A:\Sequence Listing.TXT
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```
193 Lys Gln His Met Gly Val Leu Lys Arg Val Glu Gly Lys Asp Ser Gly
194         290                 295                 300
196 Ala Asp Ile Met Gln Trp Thr Gly Pro Gly Ile Phe Thr Asp Thr Leu
197 305                 310                 315                 320
199 Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly Asp Gly
200                 325                 330                 335
202 Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr Lys Leu
203         340                 345                 350
205 Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser Glu Asp
206         355                 360                 365
208 Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro Lys Ile
209         370                 375                 380
211 Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro Asn Val
212 385                 390                 395                 400
214 Gly His Met Gly Ser Lys Ser Ser Ser Asp Arg Leu Ala Phe Val Glu
215                 405                 410                 415
217 His Leu Phe Ser Gly Ser Trp Lys Pro Lys Asn Lys
218                 420                 425
221 <210> SEQ ID NO: 3
222 <211> LENGTH: 36
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: primer 168Not-N
230 <400> SEQUENCE: 3
231 aaggaaaaaa gcggccgccg gtgaagaatg gtgtat                       36
234 <210> SEQ ID NO: 4
235 <211> LENGTH: 39
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: primer 168Not-C
243 <400> SEQUENCE: 4
244 ttttcctttt gcggccgccg ttctgtgcct gctcatgat                    39
247 <210> SEQ ID NO: 5
248 <211> LENGTH: 20
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: primer UNfor
256 <400> SEQUENCE: 5
257 ggatccccgg gtaccgagct                                         20
260 <210> SEQ ID NO: 6
261 <211> LENGTH: 20
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: primer UNrev
269 <400> SEQUENCE: 6
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RAW SEQUENCE LISTING   DATE: 08/14/2006
PATENT APPLICATION: US/10/587,956   TIME: 13:18:35

Input Set : A:\Sequence Listing.TXT
Output Set: N:\CRF4\08142006\J587956.raw

```
270 caccggtagc taatgatccc                                        20
273 <210> SEQ ID NO: 7
274 <211> LENGTH: 20
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: primer UCfor
282 <400> SEQUENCE: 7
283 cgaacatcca agtgggccga                                        20
286 <210> SEQ ID NO: 8
287 <211> LENGTH: 20
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: primer UCrev
295 <400> SEQUENCE: 8
296 ctggcgaaag ggggatgtgc                                        20
299 <210> SEQ ID NO: 9
300 <211> LENGTH: 20
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: primer 168Nfor
308 <400> SEQUENCE: 9
309 ggcggatatg gggcttcgcc                                        20
312 <210> SEQ ID NO: 10
313 <211> LENGTH: 40
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: primer 168Nrev
321 <400> SEQUENCE: 10
322 agctcggtac ccggggatcc cgttccaggg ctccacgtcc                  40
325 <210> SEQ ID NO: 11
326 <211> LENGTH: 40
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: primer 168Cfor
334 <400> SEQUENCE: 11
335 gcacatcccc ctttcgccag ccgatcacga gcttcagtcc                  40
338 <210> SEQ ID NO: 12
339 <211> LENGTH: 20
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial Sequence
343 <220> FEATURE:
344 <223> OTHER INFORMATION: primer 168Crev
347 <400> SEQUENCE: 12
348 cgtcgtccgg gcccagttcg                                        20
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VERIFICATION SUMMARY   DATE: 08/14/2006
PATENT APPLICATION: US/10/587,956   TIME: 13:18:36

Input Set : **A:\Sequence Listing.TXT**
Output Set: **N:\CRF4\08142006\J587956.raw**

L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE